

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

**Display** GenPept  all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

1: 2006271A. Reports Phe ammonia lyase...[gi:741010] [BLink](#), [Domains](#), [Links](#)

LOCUS 2006271A 725 aa linear PLN 10-JUL-1992  
 DEFINITION Phe ammonia lyase.  
 ACCESSION 2006271A  
 VERSION 2006271A GI:741010  
 DBSOURCE prf: locus 2006271A;

state: embryo;  
 taxonomy: Plantae.

KEYWORDS Phe Ammonia Lyase; Trifolium subterraneum; PAL1 Gene;  
 Acc.No.M91192; PCR Amplification; AAAIMEHI; EQHNQDV; Seq  
 Determination; 3300bp; 725AAs; DNA Blot; Multigene Family.

SOURCE Trifolium subterraneum  
 ORGANISM Trifolium subterraneum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Trifolium.

REFERENCE 1 (residues 1 to 725)

AUTHORS Howles, P.A., Arioli, T. and Weinman, J.J.

TITLE Characterization of a phenylalanine ammonia-lyase multigene family  
 in Trifolium subterraneum

JOURNAL Gene 138(1/2), 87-92 (1994)

COMMENT EC=2.3.1.74:GENE=PAL1.

FEATURES Location/Qualifiers  
 source 1..725  
 /organism="Trifolium subterraneum"  
 /db\_xref="taxon:3900"

ORIGIN

```

  1 mevvaaiilk nnindydsfc lthanannmk vnaadplnwg vaaeamkgsh ldevkrmvee
  61 yrkpvvrlgg etltisqvaiaahdgatve lsesaragvk assdwvmesm nkgtdsygv
  121 tgfagtshrr tkqggalqke lirflnagif gngtesnhtl fhtatraaml vrintllqgy
  181 sgirfeilea itkllnnnit pclplrgtit asgdlvplsy iaglltgpsn skahgpsgem
  241 llnakeafqla ginaeffelq pkeglalvng tavgsglasi vlfearnilav lsevlsaifa
  301 evmqgkpeft dhlthklkh pgqieaaaim ehlhgsayv kdakklhemd plqkpkqdry
  361 alrtspqwlq plievirst ksiereinsv ndnplidvsr nkalhggnfq gtpigvsmdn
  421 trllasigk llfaqfselv ndfynglps nlsasrnpsl dygfkgseia masycselqy
  481 lanpvtthqv saeqhnqdv slglissrkt keaieilqlm sstflialcq aidlrlhleen
  541 lknsvkntvs qvakktlig vsgelhpsrf cekdlkvvd rehvfpsyidd pcsatyplaq
  601 klrqvlvdha lvngesekns ntsifqkiat feeelktllp kevesartay engnstiank
  661 ingcrsyply kfvreelgts lltgervisp geecdklfta mcqgkiidpl lkclgewng
  721 plpic
  //
```

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for  Go Clear

Limits Preview/Index History Clipboard Details

Display GenPept Send all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**P 1: P45726. Reports Phenylalanine amm...[gi:1171998]**

BLink, Domains, Links

**LOCUS** P45726 714 aa linear PLN 01-MAY-2005  
**DEFINITION** Phenylalanine ammonia-lyase.  
**ACCESSION** P45726  
**VERSION** P45726 GI:1171998  
**DBSOURCE** swissprot: locus PALY\_CAMSI, accession P45726; class: standard.  
 created: Nov 1, 1995.  
 sequence updated: Nov 1, 1995.  
 annotation updated: May 1, 2005.  
 xrefs: D26596.1, BAA05643.1  
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948, InterProIPR001106, InterProIPR005922, PfamPF00221, TIGRFAMsTIGR01226, PROSITEPS00488

**KEYWORDS** Lyase; Phenylpropanoid metabolism.

**SOURCE** Camellia sinensis (black tea)

**ORGANISM** Camellia sinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; Ericales; Theaceae; Camellia.

**REFERENCE** 1 (residues 1 to 714)

**AUTHORS** Matsumoto,S., Takeuchi,A., Hayatsu,M. and Kondo,S.

**TITLE** Molecular cloning of phenylalanine ammonia-lyase cDNA and classification of varieties and cultivars of tea plants (*Camellia sinensis*) using the tea PAL cDNA probe

**JOURNAL** Theor. Appl. Genet. 89, 671-675 (1994)

**REMARK** NUCLEOTIDE SEQUENCE.

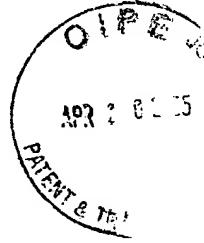
**COMMENT** STRAIN=cv. Yabukita; TISSUE=Leaf  
 [FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton.  
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH<sub>3</sub>.  
 [PATHWAY] Phenylpropanoid biosynthesis; first step.  
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).  
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity).  
 [SIMILARITY] Belongs to the PAL/histidase family.

**FEATURES** Location/Qualifiers

**source** 1..714 /organism="Camellia sinensis" /db\_xref="taxon:4442"

**gene** 1..714 /gene="PAL"

**Protein** 1..714 /gene="PAL"



Bond  
/product="Phenylalanine ammonia-lyase"  
/EC\_number="4.3.1.5"  
bond(200, 202)  
/gene="PAL"  
/bond\_type="xlink"  
/note="5-imidazolinone (Ala-Gly) (By similarity)."  
/evidence=not\_experimental  
  
Site  
201  
/gene="PAL"  
/site\_type="modified"  
/note="2,3-didehydroalanine (Ser) (By similarity)."  
/evidence=not\_experimental

## ORIGIN

1 mdsttaigng vgsggspgfc lkdplnwgva aeamkgshle evkgmveefr kpvvrlgget  
61 ltisqvaiai vrgsevavel sesaregvka ssdwvmesmn kgtdsygvtt gfgatshrrt  
121 keggalqkel irflnagifg ngteschtlp qsatraamlv rintllqgys girfeileai  
181 skflnnnitp clplrgtita sgdlvplsyi aglltgrhns kavgptgeil hpkeafrlag  
241 veggffelqp keglalvngt avgsglasmv lfeanilavl sevlsaifae vmpqkpeftd  
301 hlthklkhhp gqieaaaime hildgssyvk aaqklhemdp lqkpkqdrya lrtspqwlgp  
361 lievirsstk siereinsvn dnplinvsrn kalhggnfqg tpigvsmdnt rlavasigkl  
421 mfaqfselvn dfynnglpsn lsgrnrpsld ygfkgaeiam aaycselqfl anpvtnhvqs  
481 aeqhnqdvns lglissrkta eavdilklns stylvalcqa vdrlhfeenl rntvkstvsq  
541 vakrvltmgv ngelhpsrfc ekd1lrvvdr eyifayiddp csatyplmqk lrqvlvehal  
601 kngeseknlts tsifqkiraf eeeiktl1pk evestraaie ngnsaipnri kecrsyplyk  
661 fvreelgtel ltgekvrspg eefdkvftal ckgemidplm dclkekngap lpic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein**  for

Limits Preview/Index History Clipboard Details

Display  GenPept  Send  all to file

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

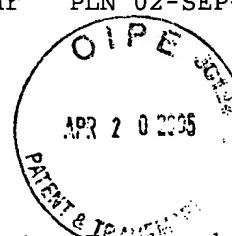
1: [CAA68938](#). Reports PAL1 protein [Pet...[gi:1524313]

BLink, Domains,  
Links

LOCUS CAA68938 716 aa linear PLN 02-SEP-1996  
 DEFINITION PAL1 protein [Petroselinum crispum].  
 ACCESSION CAA68938  
 VERSION CAA68938.1 GI:1524313  
 DBSOURCE embl locus PCPAL1, accession [Y07654.1](#)  
 KEYWORDS .  
 SOURCE Petroselinum crispum (parsley)  
 ORGANISM Petroselinum crispum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 asterids; campanulids; Apiales; Apiaceae; Apioideae; apiod  
 superclade; Apium clade; Petroselinum.  
 REFERENCE 1  
 AUTHORS Kang, X., Logemann, E. and Hahlbrock, K.  
 TITLE Cis-acting elements of the parsley pall gene  
 JOURNAL Unpublished  
 REFERENCE 2 (residues 1 to 716)  
 AUTHORS Kang, X.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-AUG-1996) X. Kang, Max-Planck-Institut, Biochemistry,  
 Carl-von-Linne-Weg 10, 50829 Cologne, FRG  
 COMMENT Related sequences X16772 (exon2), and X15473 (5'UTR and exon1).  
 FEATURES Location/Qualifiers  
 source 1..716  
 /organism="Petroselinum crispum"  
 /db\_xref="taxon:4043"  
 /clone="xk-Pcpall"  
 /cell\_line="Pc-5 /5"  
 /tissue\_type="cell suspension"  
 Protein 1..716  
 /product="PAL1 protein"  
 CDS 1..716  
 /gene="pall gene"  
 /coded\_by="join(Y07654.1:1969..2375,Y07654.1:3169..4912)"  
 /db\_xref="GOA:P24481"  
 /db\_xref="UniProt/Swiss-Prot:P24481"

## ORIGIN

1 mengngattn ghvngngmdf cmktedplyw gaaeamtgs hldevkkmva eyrkpvvk1g  
 61 getltisqva aisardgsgv tvelseaara gvkassdwvm dsmnkgtdsy gvttgfgats  
 121 hrrtkqggal qkelirflna gifgnqsdnt lphsatraam lvrin1l1gg ysgirfeile  
 181 aitkflnqni tpclplrgti tasgdlvpls yiaglltgrp nskavgptgv ilspeeafkl  
 241 agveggffel qpkeglalvn gtavgsgmas mvlfeanila vlaevmsaif aevmqgkpef  
 301 tdlthkh1kh hpgqieaaai mehildgsay vkaaqklhem dplqkpkqdr yalrtspqw1  
 361 gpqievirss tkmiereins vndnplidvs rnkaihgnf ggtpigvsmd ntlaiaaaig  
 421 klmfaqfsel vndfynnglp snlsggrnps ldygfkgaei amasycselq flanpvtvhv



481 qsaeqhnqdv ns1glissrk tseaveilk1 msttflvglc qaidlrhlee nlkstvkntv  
541 ssvakrvltm gvngelhpsr fcekdlrrvv dreyifayid dpcsatyplm qklrqtlveh  
601 alkngdnern lstsifgkia tfedelkall pkevesaraa lesgnpaipn rieecrsypl  
661 ykfvrkelgt eyltgekvts pgeefekvfi amskgeiidp llecleswng aplpic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

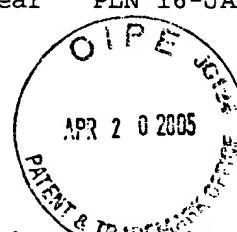
**Display** GenPept  all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

1: AAG49585. Reports phenylalanine amm...[gi:12240240]

BLink, Domains,  
Links

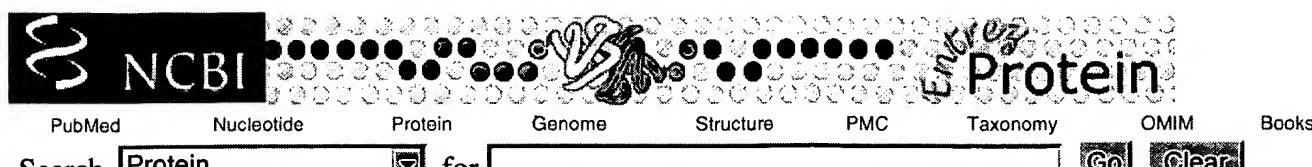
LOCUS AAG49585 711 aa linear PLN 16-JAN-2001  
 DEFINITION phenylalanine ammonia-lyase [Ipomoea nil].  
 ACCESSION AAG49585  
 VERSION AAG49585.1 GI:12240240  
 DBSOURCE locus AF325496 accession AF325496.1  
 KEYWORDS .  
 SOURCE Ipomoea nil (Japanese morning glory)  
 ORGANISM Ipomoea nil  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 asterids; lamiids; Solanales; Convolvulaceae; Ipomoeaceae; Ipomoea.  
 1 (residues 1 to 711)  
 REFERENCE 1 (residues 1 to 711)  
 AUTHORS Nakazawa,A., Nozue,M., Yasuda,H., Takeba,G. and Kubo,H.  
 TITLE Expression of phenylalanine ammonia-lyase in Pharbitis nil  
 JOURNAL Unpublished  
 REFERENCE 2 (residues 1 to 711)  
 AUTHORS Nakazawa,A., Nozue,M., Yasuda,H., Takeba,G. and Kubo,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-DEC-2000) Biology, Shinshu University, Asahi 3-1-1,  
 Matsumoto 390-8621, Japan  
 COMMENT Method: conceptual translation supplied by author.  
 FEATURES Location/Qualifiers  
 source 1..711  
 /organism="Ipomoea nil"  
 /cultivar="Violet"  
 /db\_xref="taxon:35883"  
Protein 1..711  
 /product="phenylalanine ammonia-lyase"  
 /EC\_number="4.3.1.5"  
CDS 1..711  
 /coded\_by="join(AF325496.1:1034..1419,  
 AF325496.1:2409..4158)"  
 ORIGIN  
 1 mdsvk1qmnng hqngfcvkvvd plnwevaads lrgshldevk vmvaefrkpa vklggetltv  
 61 aqvaaiasrd navtvelsee sragvkassd wvmdsmmkgt dsygvttgfg atshrrtkqg  
 121 galqkelirf lnagifgngt eschtlphsa traamlvrin tllqgysgir feileaitkl  
 181 lhnntpcpl lrqtitasgd lpvlsyiagl itgrpnskav gpnetlnae ealrlagvng  
 241 gffelqpkeg lalvngtavg sgmasmvlf eanvlavlse lsaifaevmn gkpeftdhlt  
 301 hklkhpgqi eaaaimehil dgssyvkaaq kmhemdplqk pkqdryalrt spqwlgpqie  
 361 viraatknie reinsvndnp lidvarskal hggnfqgtpi gvsmdnsrla lasigkllfa  
 421 qfslvndyy nnglpsnlta grnpsldygf kgaeiamasy cselqflanp vtnhvqsaeq  
 481 hnqdvnslgl isarktaeav dvlklmssty lvalcqaidl rfleenlrna vknavtqvak  
 541 rtlmgange lhparfcekd llrvvdreyv fayaddpcsa nyplmqklrq alvdhalqng  
 601 esekntgtsi flkvaaafede lkavlpkeve aariavesgn paipnrikec rsypllykfvr  
 661 eglgtelltg ekvrspgeec dkvftamceg siidllecl kswdgapplpi c



//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10



1: [AAL55242](#). Reports phenylalanine amm...[gi:18001007]

BLink, Domains,  
Links

LOCUS AAL55242 711 aa linear PLN 01-MAR-2005  
 DEFINITION phenylalanine ammonia-lyase [Lactuca sativa].  
 ACCESSION AAL55242  
 VERSION AAL55242.1 GI:18001007  
 DBSOURCE accession AF299330.1  
 KEYWORDS .  
 SOURCE Lactuca sativa  
 ORGANISM Lactuca sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
 Cichorieae; Lactuca.  
 REFERENCE 1 (residues 1 to 711)  
 AUTHORS Campos, R., Nonogaki, H., Suslow, T. and Saltveit, M.E.  
 TITLE Isolation and characterization of a wound inducible phenylalanine  
 ammonia-lyase gene (LsPAL1) from Romaine lettuce leaves  
 JOURNAL Physiol. Plantarum 121 (3), 429-438 (2004)  
 REFERENCE 2 (residues 1 to 711)  
 AUTHORS Campos-Vargas, R., Nonogaki, H., Suslow, T. and Saltveit, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-AUG-2000) Vegetable Crops, University of California  
 Davis, One Shields Ave., Davis, CA 95616, USA  
 COMMENT Method: conceptual translation supplied by author.  
 FEATURES Location/Qualifiers  
 source 1..711  
 /organism="Lactuca sativa"  
 /db\_xref="taxon:4236"  
Protein 1..711  
 /product="phenylalanine ammonia-lyase"  
 /name="PAL1"  
CDS 1..711  
 /coded\_by="AF299330.1:119..2254"  
 ORIGIN  
 1 mengnhvng vnelcikdpl nwgvaaealt gshldevkkm vaefrkpvvk lggetltvsq  
 61 vagiaaands dtvkvelsea aragvkassd wvmesmnkgt dsygvtgfg atshrrtkqg  
 121 galqkelirf lnagifgnqt etshtlphsa traamivrin tllqgysgir feileaitkf  
 181 lnnnitpclp lrqtitasgd lpvlsyiagl ltgrpnskav gptgevlnae kafaaagveg  
 241 gffelqpkeg lalvngtavg sgmasmvlf fd anvlallsev lsaifaevmq gkpeftdhlt  
 301 hklkhpgqi eaaaimeyil dgsdyvkaaq kvhemdplqk pkqdryalrt spqwlgpqie  
 361 virsstkmie reinsvndnp lidvsrnkal hggnfqgt pi gvsmdntrla iaaigklmfa  
 421 qfslvndfy nnqlpsnlsg grnpsldygf kggeiamasy cselqflanp vtnhvqsaeq  
 481 hnqdvnslgl isarktaeav dilklmssty lvalcqsidl rhleenmkst vkntvsqvak  
 541 kvltmgvng lhpserfcekd llrvvdreyv fayiddvcsg typlmqklrq vlvdhahnng  
 601 etekntntsi fqkiatfee lkvl1pkeve gvriayendt lsipnrikac rsyplryrfvr  
 661 eelrgfltg ekvtspgeefdrvftamckg qiidpallecl ggwngeplpi c

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

Display GenPept  all to file

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

1: O49836. Reports Phenylalanine amm...[gi:3914262] BLink, Domains, Links

LOCUS	O49836	705 aa	linear	PLN 01-MAY-2005
DEFINITION	Phenylalanine ammonia-lyase 2 (PAL-2).			
ACCESSION	O49836			
VERSION	O49836 GI:3914262			
DBSOURCE	swissprot: locus PAL2_LITER, accession <u>O49836</u> ; class: standard. created: Dec 15, 1998. sequence updated: Dec 15, 1998. annotation updated: May 1, 2005. xrefs: <u>D83076.1</u> , <u>BAA24929.1</u> , <u>JC5873</u> xrefs (non-sequence databases): HSSPP21310, InterProIPR008948, InterProIPR001106, InterProIPR005922, PfamPF00221, TIGRFAMsTIGR01226, PROSITEPS00488			
KEYWORDS	Lyase; Multigene family; Phenylpropanoid metabolism.			
SOURCE	Lithospermum erythrorhizon			
ORGANISM	<u>Lithospermum erythrorhizon</u> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamiids; Boraginaceae; <u>Lithospermum</u> .			
REFERENCE	1 (residues 1 to 705)			
AUTHORS	Yazaki, K., Kataoka, M., Honda, G., Severin, K. and Heide, L.			
TITLE	cDNA cloning and gene expression of phenylalanine ammonia-lyase in <u>Lithospermum erythrorhizon</u>			
JOURNAL	Biosci. Biotechnol. Biochem. 61 (12), 1995-2003 (1997)			
PUBMED	<u>9438980</u>			
REMARK	NUCLEOTIDE SEQUENCE.			
COMMENT	On Apr 12, 2005 this sequence version replaced gi:7437121. [FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton. [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH <sub>3</sub> . [PATHWAY] Phenylpropanoid biosynthesis; first step. [SUBCELLULAR LOCATION] Cytoplasmic (Probable). [TISSUE SPECIFICITY] Expressed mainly in roots. [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity). [SIMILARITY] Belongs to the PAL/histidase family.			
FEATURES	Location/Qualifiers			
source	1..705 <u>/organism="Lithospermum erythrorhizon"</u> <u>/db_xref="taxon:34254"</u>			
Protein	1..705 <u>/product="Phenylalanine ammonia-lyase 2"</u> <u>/EC_number="4.3.1.5"</u>			

Bond bond(191,193)  
/bond\_type="xlink"  
/note="5-imidazolinone (Ala-Gly) (By similarity)."  
/evidence=not\_experimental  
Site 192  
/site\_type="modified"  
/note="2,3-didehydroalanine (Ser) (By similarity)."  
/evidence=not\_experimental

## ORIGIN

1 mengngkmef cmkdplnwgm aaesmkgschl devkkmvaef rkpvvqlagk tltiaqvaai  
61 aarddgvtve laeaaregvk assdwvmesm nkgtdsygvt tgfatshrr tkqggalqke  
121 lirflnagif gngtetshtl phsattraaml vrintllqgy sgirfeilea itkflnnit  
181 pclplrgtit asgdlvplsy iaglltgrpn skavgptgek lnaeeafrla gissgffelq  
241 pkeglalvng tavsgasm vlyeanilgv msevlsavfa evmngkpeft dhlthklkh  
301 pgqieaaaim ehildgsgyv kaaellhemd plqpkqdry alrtspqwlg pqievirsat  
361 kmiereinsv ndnplidvsr nkalhggnfq gtpigvamdn trlaiaaaigk llfaqfselv  
421 ndyynnglps nltgsrdpsl dygfkgaeia masycselqf lanpvtvhvq saeqhnqdv  
481 slglissrkt seaveilk lm sssflvalcq avdlrhieen vrlavkkts qvakktlnig  
541 vdgvlhpsrf sekellrvvd reyvfayadd pcsatyplmq klrevlvsha lansgnekda  
601 stsifhkigv feeelkgilp kevenaravv engtpaipnk ieecrsyply kfvrgegte  
661 lltgekvrsp geeldqvfna lcegklvdpl lacleawnga plpic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

GenPept  all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

1: Q42858. Reports Phenylalanine amm...[gi:3024361] BLink, Domains, Links

LOCUS Q42858 708 aa linear PLN 01-MAY-2005  
 DEFINITION Phenylalanine ammonia-lyase.  
 ACCESSION Q42858  
 VERSION Q42858 GI:3024361  
 DBSOURCE swissprot: locus PAL2\_IPOBA, accession Q42858;  
 class: standard.  
 created: Jul 15, 1998.  
 sequence updated: Jul 15, 1998.  
 annotation updated: May 1, 2005.  
 xrefs: D78640.1, BAA11459.1, T10909  
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,  
 InterProIPR001106, InterProIPR005922, PfamPF00221,  
 TIGRFAMsTIGR01226, PROSITEPS00488  
 KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.  
 SOURCE Ipomoea batatas (sweet potato)  
 ORGANISM Ipomoea batatas Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.  
 REFERENCE 1 (residues 1 to 708)  
 AUTHORS Tanaka, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (??-DEC-1995)  
 REMARK NUCLEOTIDE SEQUENCE.  
 STRAIN=cv. Beniazuma; TISSUE=Root  
 COMMENT On Apr 12, 2005 this sequence version replaced gi:7437130.  
 [FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton.  
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).  
 [PATHWAY] Phenylpropanoid biosynthesis; first step.  
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).  
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity).  
 [SIMILARITY] Belongs to the PAL/histidase family.  
 FEATURES Location/Qualifiers  
 source 1..708  
 /organism="Ipomoea batatas"  
 /db\_xref="taxon:4120"  
Protein 1..708  
 /product="Phenylalanine ammonia-lyase"  
 /EC\_number="4.3.1.5"  
 Bond bond(194,196)  
 /bond\_type="xlink"

  
APR 20 2005

/note="5-imidazolinone (Ala-Gly) (By similarity)."  
/evidence=not\_experimental  
Site  
195  
/site\_type="modified"  
/note="2,3-didehydroalanine (Ser) (By similarity)."  
/evidence=not\_experimental

## ORIGIN

1 megaianght ndfcikvdpl nwemaadslk gshldevkrm vaefrnpavk iggqtltslr  
61 sppiaardna skwssprlpa rresssdwvm nsmnnngtdsy gvttgfgats hrrtknghal  
121 qqelirflna gifgtgtgas htlphsatra amlvrintll qgysgirfei leaitkllnh  
181 nitpc1plrg titasgdlvp lsyiaglltg rpnskavgpn gealtaeeaf klagvqggff  
241 elqpkeglal vngtavgsgm asmvlfeanv lavlsevla ifaevmngkp eftdhltkl  
301 khpgqieaa aimehildrs yymkaaqkhh emdplqkpkq dryalrtspq wlqpqievir  
361 qatkmierei nsvndnplid vsrnkalhgg nfqqtpigvs mdnsrlalas igklifaqfs  
421 elvndyyynng lpsnltagrn psldygfkvg eiamasycse lqflanpvtn hvqsaeqhng  
481 dvns1glisa rktaeavdvl klmsstylva lcqaidlrhl eenlknavrн tvnqvakrtl  
541 tmgvngelhp srfcekdlr vvdreyvfay addpcsanyp lfqklrqqlv dhalqngehe  
601 knvstsifqk iaafedelka vlpkevegar saiengnpai pnritecrsy plykfvreel  
661 gtemltgekv kspgevcdkv ftavcdggii dplleclksw dgap1pic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

**Display** GenPept  all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**P19142: Reports Phenylalanine amm...[gi:129585]**

**BLink, Domains, Links**

**LOCUS** P19142 712 aa linear PLN 01-MAY-2005

**DEFINITION** Phenylalanine ammonia-lyase class II.

**ACCESSION** P19142

**VERSION** P19142 GI:129585

**DBSOURCE** swissprot: locus PAL2\_PHAVU, accession P19142; class: standard.  
created: Nov 1, 1990.  
sequence updated: Nov 1, 1990.  
annotation updated: May 1, 2005.  
xrefs: S04127  
xrefs (non-sequence databases): HSSPP21310, InterProIPR008948, InterProIPR001106, InterProIPR005922, PfamPF00221, TIGRFAMsTIGR01226, PROSITEPS00488

**KEYWORDS** Lyase; Multigene family; Phenylpropanoid metabolism.

**SOURCE** Phaseolus vulgaris

**ORGANISM** Phaseolus vulgaris Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilioideae; Phaseoleae; Phaseolus.

**REFERENCE** 1 (residues 1 to 712)

**AUTHORS** Cramer,C.L., Edwards,K., Dron,M., Liang,X., Dildine,S.L., Bolwell,G.P., Dixon,R.A., Lamb,C.J. and Schuch,W.

**TITLE** Phenylalanine ammonia-lyase gene organisation and structure

**JOURNAL** Plant Mol. Biol. 12, 367-383 (1989)

**REMARK** NUCLEOTIDE SEQUENCE.

**COMMENT** On Apr 12, 2005 this sequence version replaced gi:81877.  
[FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton.  
[CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH<sub>3</sub>.  
[PATHWAY] Phenylpropanoid biosynthesis; first step.  
[SUBCELLULAR LOCATION] Cytoplasmic (Probable).  
[PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity).  
[SIMILARITY] Belongs to the PAL/histidase family.

**FEATURES** Location/Qualifiers

**source** 1..712  
/organism="Phaseolus vulgaris"  
/db\_xref="taxon:3885"

**Protein** 1..712  
/product="Phenylalanine ammonia-lyase class II"  
/EC\_number="4.3.1.5"

**Bond** bond(198,200)



/bond\_type="xlink"  
/note="5-imidazolinone (Ala-Gly) (By similarity)."  
/evidence=not\_experimental  
Site 199  
/site\_type="modified"  
/note="2,3-didehydroalanine (Ser) (By similarity)."  
/evidence=not\_experimental  
ORIGIN  
1 mdatpngkda fvtaanaag dplnwaaaae alsghldev krmvaeyrkp avrlggqtlt  
61 iaqvaataah dqglkvelae saracvkais dwvmesmdkg tdsygitgf gatshrrtkq  
121 ggalqkelir flnagifgng tesnctlph atraamlrvv ntllqgysgi rfeileaitk  
181 llnnnitpcl plrgtitasg dlvplesiyag lltgrpnska vgpsgeilna keafelanig  
241 seffelqpke glalvngtav gsglasivlf eanilavlse visaifaevm qgkpeftdhl  
301 thklkhpgq ieaaaimehi ldgssyikaa kklheidplq kpkqdryalr tspqwlqpqi  
361 evirfstksi ereinsvndn plisvsrnka lhgnfqqtp igvsmdntrl aiasigklmf  
421 aqfsdlvndy ynnglpsnlr asrnpsldyg fkgaeiamas ycselqylan pvtshvqsae  
481 qhnqdvnslg lissrktnea leilklnsst fvalcqaid lrhleenlkn tvknvvsvqa  
541 krtlttgvng elhpsrfcek allkvverey tfayiddpcs gtyplmgklr qvlvdylan  
601 geneknlnts ifqkiasfee elktllpkev egarlayend qcaipnkikd crsyplykfv  
661 reelgtsllt gekvispgce cdkvfsamcq gkiidpllec lgewngaplp ic  
//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for **Go** **Clear**

Limits Preview/Index History Clipboard Details

Display GenPept

Send all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**1: CAA57057. Reports phenylalanine amm...[gi:535008]**

BLink, Domains,  
Links

LOCUS CAA57057 718 aa linear PLN 07-DEC-1994  
 DEFINITION phenylalanine ammonia-lyase 3 [Petroselinum crispum].  
 ACCESSION CAA57057  
 VERSION CAA57057.1 GI:535008  
 DBSOURCE embl locus PCPAL3, accession X81159.1  
 KEYWORDS .  
 SOURCE Petroselinum crispum (parsley)  
 ORGANISM Petroselinum crispum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 asterids; campanulids; Apiales; Apiaceae; Apioideae; apiod  
 superclade; Apium clade; Petroselinum.  
 REFERENCE 1  
 AUTHORS Appert,C., Logemann,E., Hahlbrock,K., Schmid,J. and Amrhein,N.  
 TITLE Structural and catalytic properties of the four phenylalanine  
 ammonia-lyase isoenzymes from parsley (Petroselinum crispum Nym.)  
 JOURNAL Eur. J. Biochem. 225 (1), 491-499 (1994)  
 PUBMED 7925471  
 REFERENCE 2 (residues 1 to 718)  
 AUTHORS Appert,C.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-AUG-1994) C. Appert, Institut fuer  
 Pflanzenwissenschaften, Eidgenoessische Technische Hochschule,  
 Zuerich, Universitaetsstrasse 2, 8092 Zurich, SWITZERLAND  
 FEATURES Location/Qualifiers  
 source 1..718  
 /organism="Petroselinum crispum"  
 /db\_xref="taxon:4043"  
 Protein 1..718  
 /product="phenylalanine ammonia-lyase 3"  
 /EC\_number="4.3.1.5"  
 CDS 1..718  
 /gene="PAL3"  
 /coded\_by="X81159.1:89..2245"  
 /note="tetramere subunit"  
 /db\_xref="GOA:P45729"  
 /db\_xref="UniProt/Swiss-Prot:P45729"  
 ORIGIN

1 mayvngttng hangnqlldlc mkkedplnwg vaaealtgsh ldevkrmvae yrkpvvkleg  
 61 etltisqva isarddsgvk velseearag vkassdwvmd smnkgtdsyg vttgfgatsh  
 121 rrtkqggalq kelirflnag ifgsgaeagn ntlphsatra amlvrinll qgysgirfei  
 181 leaitkflnh nitpclplrg titasgdlvp lsyiaglltg rpnskavgpt gvtlspeeaf  
 241 klagveggff elqpkeglal vngtavgsgm asmvlfteani lavlaevmsa ifaevmqgkp  
 301 eftdhltkhl khpgqgieaa aimehildgs ayvkaaqklh emdplqkpkq dryalrtspq  
 361 wlqpqievir sstkmierei nsvndnplid vsrnkaihgg nfqgspigvs mdntrlaiaa

421 igklmfaqfs elvndfynng lpsnlsggrn psldygfkga eiamasycse 1qflanpvt  
481 hvqsaeqhnq dvnslgli ss rktseaveil klmsttflvg lcqaidlrhl eenlkstvkn  
541 tvsqvakrvl tmgvngelhp srfcekdlr vvdreyifay iddpcsatyp lmqklretlv  
601 ehalnngdke rn1stsifqk iaafedelka llpkevetar aalesgnpai pnrikecrsy  
661 plykfvreel gteyltgekv rspgeefekv ftamskgeii dplleclesw ngaplpic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

**Display** GenPept  **Send** all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**1: AAF40224. Reports phenylalanine amm...[gi:7208616]**

BLink, Domains, Links

LOCUS AAF40224 730 aa linear PLN 19-SEP-2001

DEFINITION phenylalanine ammonia-lyase 2 [Rubus idaeus].

ACCESSION AAF40224

VERSION AAF40224.1 GI:7208616

DBSOURCE locus AF237955 accession AF237955.1

KEYWORDS .

SOURCE Rubus idaeus

ORGANISM Rubus idaeus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rubus.

REFERENCE 1 (residues 1 to 730)

AUTHORS Kumar, A. and Ellis, B.E.

TITLE The phenylalanine ammonia-lyase gene family in raspberry. Structure, expression, and evolution

JOURNAL Plant Physiol. 127 (1), 230-239 (2001)

PUBMED 11553751

REFERENCE 2 (residues 1 to 730)

AUTHORS Kumar, A. and Ellis, B.E.

TITLE Direct Submission

JOURNAL Submitted (23-FEB-2000) The Biotechnology Laboratory and Faculty of Agricultural Sciences, University of British Columbia, 344-2357 Main Mall, Vancouver, BC V6T 1Z4, Canada

COMMENT Method: conceptual translation supplied by author.

FEATURES Location/Qualifiers

source 1..730

/organism="Rubus idaeus"

/db\_xref="taxon:32247"

/dev\_stage="fruit"

Protein 1..730

/product="phenylalanine ammonia-lyase 2"

/EC\_number="4.3.1.5"

/name="PAL; phenylpropanoid; multigene; flavonoid"

CDS 1..730

/gene="PAL2"

/coded\_by="AF237955.1:66..2258"

ORIGIN

1 mesitqnggh hqngiqngsl ddglciktes iktgysvsdp lnwgaaaesm tgshldevrr  
 61 mvaeyrkpvv klggetltis qvaaianhds gvkvelaesa ragvkassdw vmdsmnkgt  
 121 sygvttgfga tshrrtkqga alqkelirfl nagvlrngte sahtlphsat raamlvrint  
 181 llqgqsgirf eileaiskfl nhnitpclpl rgtitasgdl vplsyiagll tgrpnskavg  
 241 pkgetlnaae afaqvgissg ffelqpkegl alvngtavgs glastvlvet nilallseil  
 301 saifaevmqg kpeftdhlt klkhpgqie aaaimehild gssyvkaaek lheqdplqkp  
 361 kqdralrts pqwlgpqiev irfstksier einsvndnpl idvsrnkalh ggnfqgtpig  
 421 vsmdntrlai asigklmfaq fselvndfyn nglpsnlsgg rdpsldygfk gaeiamasyc



481 selqflanpv tnhvqsaeqh nqdvnslgli ssrktaeavd ilklmsstfl valcqaidlr  
541 hleenlkstv kntvsqqlakr vlttgvngel hpsrfcekd1 lmvereylf ayiddpcsat  
601 yplmqrlrqv lvehaltnge neknastsif qkitafeeel ktilpkveves araayesgna  
661 aipnrivecr syplykfvre elggefltge kvrspgeecd kvftamcqgn iidpildcls  
721 gwngeplpic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

Display GenPept  all to file

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

1: P35510. Reports Phenylalanine amm...[gi:1171991] BLink, Domains, Links

LOCUS	P35510	725 aa	linear	PLN 01-MAY-2005
DEFINITION	Phenylalanine ammonia-lyase 1.			
ACCESSION	P35510			
VERSION	P35510 GI:1171991			
DBSOURCE	swissprot: locus PAL1_ARATH, accession <u>P35510</u> ; class: standard. extra accessions:Q9ZQD6, created: Jun 1, 1994. sequence updated: Nov 1, 1995. annotation updated: May 1, 2005. xrefs: <u>L33677.1</u> , <u>AAC18870.1</u> , <u>AC006922.7</u> , <u>AAM15324.1</u> , <u>X62747.1</u> , <u>CAA44609.1</u> , <u>S52990</u> xrefs (non-sequence databases): HSSPP21310, InterProIPR008948, InterProIPR001106, InterProIPR005922, PfamPF00221, TIGRFAMsTIGR01226, PROSITEPS00488			
KEYWORDS	Lyase; Multigene family; Phenylpropanoid metabolism.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	<u>Arabidopsis thaliana</u> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1 (residues 1 to 725)			
AUTHORS	Wanner, L.A., Li, G., Ware, D., Somssich, I.E. and Davis, K.R.			
TITLE	The phenylalanine ammonia-lyase gene family in <i>Arabidopsis thaliana</i>			
JOURNAL	Plant Mol. Biol. 27 (2), 327-338 (1995)			
PUBMED	<u>7888622</u>			
REMARK	NUCLEOTIDE SEQUENCE. STRAIN=cv. Landsberg erecta			
REFERENCE	2 (residues 1 to 725)			
AUTHORS	Lin, X., Kaul, S., Rounsley, S., Shea, T.P., Benito, M.I., Town, C.D., Fujii, C.Y., Mason, T., Bowman, C.L., Barnstead, M., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J., Ronning, C.M., Koo, H.L., Moffat, K.S., Cronin, L.A., Shen, M., Pai, G., Van Aken, S., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Venter, J.C.			
TITLE	Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i>			
JOURNAL	Nature 402 (6763), 761-768 (1999)			
PUBMED	<u>10617197</u>			
REMARK	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. STRAIN=cv. Columbia			
REFERENCE	3 (residues 1 to 725)			
AUTHORS	Ohl, S., Hedrick, S.A., Chory, J. and Lamb, C.J.			
TITLE	Functional properties of a phenylalanine ammonia-lyase promoter			

JOURNAL from Arabidopsis  
 Plant Cell 2 (9), 837-848 (1990)

PUBMED 2152131

REMARK NUCLEOTIDE SEQUENCE OF 1-240.  
 STRAIN=cv. Columbia

COMMENT On or before Apr 12, 2005 this sequence version replaced  
gi:1076369, gi:548456.

[FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton.

[CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH(3).

[PATHWAY] Phenylpropanoid biosynthesis; first step.

[SUBCELLULAR LOCATION] Cytoplasmic (Probable).

[PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity).

[SIMILARITY] Belongs to the PAL/histidase family.

**FEATURES** Location/Qualifiers

<u>source</u>	1..725 <i>/organism="Arabidopsis thaliana"</i> <i>/db_xref="taxon:3702"</i>
<u>gene</u>	1..725 <i>/gene="PAL1"</i> <i>/locus_tag="At2g37040"</i> <i>/note="synonym: T1J8.22"</i>
<u>Protein</u>	1..725 <i>/gene="PAL1"</i> <i>/locus_tag="At2g37040"</i> <i>/product="Phenylalanine ammonia-lyase 1"</i> <i>/EC_number="4.3.1.5"</i>
<u>Bond</u>	bond(211,213) <i>/gene="PAL1"</i> <i>/locus_tag="At2g37040"</i> <i>/bond_type="xlink"</i> <i>/note="5-imidazolinone (Ala-Gly) (By similarity)."</i> <i>/evidence=not_experimental</i>
<u>Site</u>	212 <i>/gene="PAL1"</i> <i>/locus_tag="At2g37040"</i> <i>/site_type="modified"</i> <i>/note="2,3-didehydroalanine (Ser) (By similarity)."</i> <i>/evidence=not_experimental</i>
<u>Region</u>	329 <i>/gene="PAL1"</i> <i>/locus_tag="At2g37040"</i> <i>/region_name="Conflict"</i> <i>/note="V -&gt; I (in Ref. 2)."</i> <i>/evidence=experimental</i>
<u>Region</u>	426 <i>/gene="PAL1"</i> <i>/locus_tag="At2g37040"</i> <i>/region_name="Conflict"</i> <i>/note="R -&gt; A (in Ref. 2)."</i> <i>/evidence=experimental</i>
<u>Region</u>	612 <i>/gene="PAL1"</i> <i>/locus_tag="At2g37040"</i> <i>/region_name="Conflict"</i> <i>/note="V -&gt; I (in Ref. 2)."</i> <i>/evidence=experimental</i>

## ORIGIN

1 meingahksn gggvdamlcg gdiktknmvi naedplnwga aaeqmkgs1 devkrmvae  
61 rkpvvnlge tltigqvaai stignsvkve lsetaragvn assdwvmesm nkgttdsygvt  
121 tgfagtshrr tkngvalqke lirflnagif gsketsht1 phsattraam1 vrintllqgf  
181 sgirfeilea itsflnnnit ps1plrgtit asgd1lp1sy iaglltgrpn skatgpngea  
241 ltaeeafkla gissgffd1q pkeglalvng tavgsgmasm vlfetnv1sv laeilsavfa  
301 evmsgkpeft dhlthrlkh1 pgqieaaavm ehildgssym klagklhemd plqpkqdry  
361 alrtspqwlg pqieviryat ksiereinsv ndnplidvsr nkaihgnfq gtpigvsmdn  
421 trlairaigk lmfaqfse1v ndfyngn1ps nltasrnps1 dygfkgaeia masycselqy  
481 lanpvtshvq saeqhnqdvn slglissrkt seavdilk1m sttf1vlaicq avdlrhleen  
541 lrqtvkntvs qvakvl1tg vngelhpsrf cekdl1kvvd reqvytyadd pcsatypliq  
601 klrqvivdha lvngesekna vtsifhkiga feeelkav1p keveaaraay dngtsaipnr  
661 ikecrsypl1 rvfreelg1e lltgekvtsp geefdkvfta icegkiidpm meclnewnga  
721 pipic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI**  

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein**  for

[Limits](#)[Preview/Index](#)[History](#)[Clipboard](#)[Details](#)[Display](#)[GenPept](#)[Send](#)[all to file](#)Range: from to Features:  SNP  CDD  MGC  HPRD  STS**1:** [CAA35886. Reports phenylalanine amm...\[gi:3294\]](#)[BLink](#), [Domains](#),  
[Links](#)

LOCUS CAA35886 716 aa linear PLN 28-NOV-1996  
 DEFINITION phenylalanine ammonia-lyase [Rhodosporidium toruloides].  
 ACCESSION CAA35886  
 VERSION CAA35886.1 GI:3294  
 DBSOURCE embl locus RTPAL2, accession [X51513.1](#)  
 KEYWORDS .  
 SOURCE Rhodosporidium toruloides  
 ORGANISM Rhodosporidium toruloides  
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;  
 Microbotryomycetidae; Sporidiobolales; Rhodosporidium.  
 REFERENCE 1 (residues 1 to 716)  
 AUTHORS Rasmussen,O.F. and Oerum,H.  
 TITLE Analysis of the gene for phenylalanine ammonia-lyase from  
 Rhodosporidium toruloides  
 JOURNAL DNA Seq. 1 (3), 207-211 (1991)  
 PUBMED [1773059](#)  
 REFERENCE 2 (residues 1 to 716)  
 AUTHORS Petersen,S.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JAN-1990) Petersen S.K., Genetic Engineering Group,  
 Technical University of Denmark, Building 227, DK 2800 Lyngby,  
 Denmark  
 COMMENT See also <M18261> for R.toruloides strain IFO 0559 pal gene.  
 FEATURES Location/Qualifiers  
 source 1..716  
 /organism="Rhodosporidium toruloides"  
 /strain="CBS 14"  
 /db\_xref="taxon:5286"  
 /clone\_lib="Centralbureau voor Schimmelcultures"  
 Protein 1..716  
 /product="phenylalanine ammonia-lyase"  
 CDS 1..716  
 /gene="pal"  
 /coded\_by="join(X51513.1:519..829,X51513.1:919..1005,  
 X51513.1:1067..1201,X51513.1:1259..1835,  
 X51513.1:1897..2063,X51513.1:2123..2411,  
 X51513.1:2468..3052)"  
 /db\_xref="GOA:P11544"  
 /db\_xref="UniProt/Swiss-Prot:[P11544](#)"

**ORIGIN**

```

  1 mapsldish sfangvasak qavngastnl avagshlptt qvtqvdivvek mlaaptdstl
  61 eldgyslnlg dvvsarkgr pvrkdsdei rskidsvef lrsqlsmssv gvttgfggsa
  121 dtrtedaisl qkallehqlc gvpssfdsf rlrglensl plevvrgamt irvnsltrgh
  181 savrlvvlea ltnflnhgit pivplrgtis asgdlsplsy iaaaaisghpd skvhvvhegk
  241 ekilyaream alfnlepvvl gpkeglglvn gtavsasmat lalhdahmls llsqsltam

```

301 veamvghags fhpflhdvtr phptqievag nirklegsr favhheeevk vkkdddegilrq  
361 dryplrtspq wlgplvsdli hahavltiea gqsttdnpli dvenktshhg gnfqaaavan  
421 tmeektrlgla qigklnftql temlnagmn rglpsclaaed pslyhckgl diaaaaaytse  
481 lghlanpvtt hvqpaemang avnslalisa rrttesndvl slllathlyc vlqaidlrai  
541 efefkkqfgp aivslidqh fgsamtgsnlr delvekvnk t lakovleqtns ydlvprwhda  
601 fsfaagtvee vlsststs la avnawkvaaa esaisltrqv retfwsaast sspalsylsp  
661 rtqilyafvr eelgvkarr dvflgkqevt igsnvskiye aiksgrinnv llkmla

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI**   

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein**  for

[Limits](#)[Preview/Index](#)[History](#)[Clipboard](#)[Details](#)[Display](#)[GenPept](#)[Send](#)[all to file](#)Range: from to Features:  SNP  CDD  MGC  HPRD  STS 1: [AAA33883](#). Reports phenylalanine amm...[gi:169746][BLink](#), [Domains](#),  
[Links](#)

LOCUS AAA33883 693 aa linear PLN 27-APR-1993

DEFINITION phenylalanine ammonia-lyase.

ACCESSION AAA33883

VERSION AAA33883.1 GI:169746

DBSOURCE locus RHDPAL accession [M18261.1](#)

KEYWORDS

SOURCE Rhodosporidium toruloides

ORGANISM Rhodosporidium toruloidesEukaryota; Fungi; Basidiomycota; Urediniomycetes;  
Microbotryomycetidae; Sporidiobolales; Rhodosporidium.

REFERENCE 1 (residues 1 to 693)

AUTHORS Anson,J.G., Gilbert,H.J., Oram,J.D. and Minton,N.P.

TITLE Complete nucleotide sequence of the Rhodosporidium toruloides gene  
coding for phenylalanine ammonia-lyase

JOURNAL Gene 58 (2-3), 189-199 (1987)

PUBMED [2828184](#)

COMMENT Method: conceptual translation.

FEATURES Location/Qualifiers

source

1..693  
/organism="Rhodosporidium toruloides"  
/db\_xref="taxon:5286"

Protein

1..693  
/name="phenylalanine ammonia-lyase"

CDS

1..693  
/coded\_by="join(M18261.1:354..595,M18261.1:687..773,  
M18261.1:835..969,M18261.1:1027..1603,M18261.1:1665..1831,  
M18261.1:1891..2179,M18261.1:2236..2820)"

ORIGIN

```

1 maprptsqsg artcpttqvt qvdivekmla aptdstleld gyslnlgdvv saarkgrpvr
61 vkdsdeirsk idksveflrs qlsmssvygvt tgfggsadtr tedaislqka llehqlcgvl
121 pssfdsfrlg rglenslple vvrgamtirv nsltrghsav rlvvlealtn flnhgitpiv
181 plrgtisasp dlsplsyiaa aisghpdskv hvghegkeki lyareamalf nlepvvlgpk
241 eglglvngta vsasmatlal hdahmlslls qsltamtvea mvghagsfhp flhdvtrphp
301 tqievagnir kllegsrav hhheeekvkvd degilrqdry plrtspqwlg plvsdliahah
361 avltieagqs ttdnplidve nktshggmf qaaavantme ktrlglaqig klnftqltem
421 lnagmnrglp sclaaedpsl syhckgldia aaaytselgh lanpvtthvq paemanqavn
481 slalisarrt tesndvlsll lathlycvlq aidlraiefe fkkqfgpaiv slidqhfgsa
541 mtgsnrlrdel vekvnkltak rleqtnsydl vprwhdafsf aagtvvevls stslslaavn
601 awkvaaaesa isltrqvret fwsaastssp alsylsprtg ilyafvreel gvkarrgdvf
661 lgkgevtigs nvskiyeik sgrinnvllk mla

```

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for **Go** **Clear**

Limits Preview/Index History Clipboard Details

Display GenPept Send all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

1: 1314202A. Reports Phe ammonia lyase...[gi:225818]

BLink, Domains, Links

LOCUS 1314202A 705 aa linear PLN 05-APR-1996  
 DEFINITION Phe ammonia lyase.  
 ACCESSION 1314202A  
 VERSION 1314202A GI:225818  
 DBSOURCE prf: locus 1314202A;

state: glioblastoma derived T cell;  
 taxonomy: Fungi.

KEYWORDS Phe Ammonia Lyase; pal Gene; Rhodosporidium toruloides;  
 cDNA/Genomic Clone; Seq Determination; 2980bp; 582AAs; Exon x7; Seq  
 Comparison; Codon Usage.

SOURCE Rhodosporidium toruloides

ORGANISM Rhodosporidium toruloides  
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;  
 Microbotryomycetidae; Sporidiobolales; Rhodosporidium.

REFERENCE 1 (residues 1 to 705)

AUTHORS Anson,J.G., Gilbert,H.J., Oram,J.D. and Minton,N.P.

TITLE Complete nucleotide sequence of the Rhodosporidium toruloides gene  
 coding for phenylalanine ammonia-lyase

JOURNAL Gene 58(2/3), 189-199 (1987)

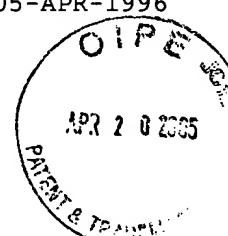
COMMENT gene.pal exon.x7.

FEATURES Location/Qualifiers  
 source 1..705  
 /organism="Rhodosporidium toruloides"  
 /db\_xref="taxon:5286"

ORIGIN

```

  1 maprptsqsq artcpttqvt qvdivekmla aptdstleld gyslnlgdvv saarkgrpvr
  61 vkdsdeirsk idksveflrs qlsmsvygvt tgfggssadtr tedaislqka llehqda1sl
  121 qkalcvlps sfdsfrlrgc lenslplevv rgamtirvns ltrghsavrl vvlealtnfl
  181 nhgitpivpl rgtisasgdl sply siaai sghpdskvhv vhegkekily areamalfn1
  241 epvvlgpkeg lglvngtavs asmatlalhd ahmlsllsq5 ltamtveamv ghagsfhpf1
  301 hdvtrphptq ievagnirk1 legsrfavhh eeevkvdde gilrqdrypl rtspqwl1gpl
  361 vsdlihahav ltieaggstt dnplidvenk tshhgnfqa aavantmekt rlqlaqigkl
  421 nftqltemln agmnrglpsc laaaedpslsy hckgldiaaa aytse1gh1l nftanpvtt
  481 vqpaemanga vnsalalisar rttesndvls l1lathlycv lqaidlraie fekkqfgpa
  541 ivs1idqhfg samtgsnlrd elvekvnk1 akrleqtnsy dlvprwhdaf sfaagtvvve
  601 lsststs1laa vnawkvaaae saisltrqvr etfwsaasts spalsylspr tqilyafvre
  661 elgvkarrgd vflgkqevti gsnvskiyea iksgrinnvl lkmla
  //
```



[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for  Go Clear

Limits Preview/Index History Clipboard Details

Display GenPept  Send all to file

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

1: [CAA31486. Reports phenylalanine amm...\[gi:295942\]](#) [BLink](#), [Domains](#), [Links](#)

**LOCUS** CAA31486 713 aa linear PLN 30-MAR-1999  
**DEFINITION** phenylalanine ammonia-lyase [Rhodotorula mucilaginosa].  
**ACCESSION** CAA31486  
**VERSION** CAA31486.1 GI:295942  
**DBSOURCE** embl locus RRPAL, accession [X13094.1](#)  
**KEYWORDS**.  
**SOURCE** Rhodotorula mucilaginosa  
**ORGANISM** Rhodotorula mucilaginosa  
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;  
 Microbotryomycetidae; Sporidiobolales; mitosporic Sporidiobolales;  
 Rhodotorula.  
**REFERENCE** 1  
**AUTHORS** Filpula,D., Vaslet,C.A., Levy,A., Sykes,A. and Strausberg,R.L.  
**TITLE** Nucleotide sequence of gene for phenylalanine ammonia-lyase from Rhodotorula rubra  
**JOURNAL** Nucleic Acids Res. 16 (23), 11381 (1988)  
**PUBMED** [3205749](#)  
**REFERENCE** 2 (residues 1 to 713)  
**AUTHORS** Filpula,D.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (28-SEP-1988) Filpula D., Genex Corporation, 16020 Industrial Drive, Gaithersburg, MD 20877, USA  
**FEATURES** Location/Qualifiers  
**source** 1..713  
 /organism="Rhodotorula mucilaginosa"  
 /strain="NRRLY-15597"  
 /db\_xref="taxon:5537"  
**Protein** 1..713  
 /product="phenylalanine ammonia-lyase"  
**CDS** 1..713  
 /gene="PAL"  
 /coded\_by="join(X13094.1:646..974,X13094.1:1062..1148,  
 X13094.1:1231..1930,X13094.1:2011..2177,  
 X13094.1:2247..2409,X13094.1:2484..3179)"  
 /db\_xref="GOA:P10248"  
 /db\_xref="UniProt/Swiss-Prot:P10248"  
**ORIGIN**  
 1 mapsvdsiat svanslsngl haaaaanggd vhkktagags llpttettql diverilada  
 61 gatdqikldg ytltdgvvg aarrgrsvkv adsphireki dasveflrtq ldnsvygvtt  
 121 gfggsadtrt edaislqkal lehqlcgvlp tsmdgfalgr glenslplev vrgamtirvn  
 181 sltrghsavv ivvlealtnf lnhgtpivp lrqtisasd 1splsyiaas itghpdskvh  
 241 vdgkimsaqe aialkgqv vlgpkeglgl vngtavasm atlaltdahv lsllaqalta  
 301 ltveamvgha gsfhpflhdv trphptqiev arnirtlleg skyavhhete vkvkddiegil  
 361 rqdryplrcs pqwlglvsd mihahavls1 eaggsttdnp lidlenkmth hggafmassv  
 421 gntmektrla valmgkvsft qltemlnagm nralpsclaa edpslsyhck gldiaaaaayt

481 selghlanpv sthvqpaemg nqainslali sarrtaeand vlslllathl ycvlgavdlr  
541 amefehtkaf epmvte1kq hfgalataev edkvrksiyk rlqqnnnsydl eqrwhdtfsv  
601 atgavveala ggevslasln awkvacaeka ialtrsvrds fwaapssssp alkylsprtr  
661 vlysfvreev gvkarrgdvy lgkqevtigt nvsriyeaik sgciapvlvk mma

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

**Display** GenPept  all to file

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

1: [CAA09013](#). Reports phenylalanine amm...[gi:4127289]

BLink, Domains,  
Links

LOCUS CAA09013 740 aa linear PLN 15-APR-2005  
 DEFINITION phenylalanine ammonium lyase [Amanita muscaria].  
 ACCESSION CAA09013  
 VERSION CAA09013.1 GI:4127289  
 DBSOURCE embl locus AAJ10143, accession [AJ010143.1](#)  
 KEYWORDS .  
 SOURCE Amanita muscaria (fly agaric)  
 ORGANISM Amanita muscaria  
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 Agaricales; Amanitaceae; Amanita.  
 REFERENCE 1  
 AUTHORS Nehls, U., Ecke, M. and Hampp, R.  
 TITLE Sugar- and nitrogen-dependent regulation of an Amanita muscaria  
 phenylalanine ammonium lyase gene  
 JOURNAL J. Bacteriol. 181 (6), 1931-1933 (1999)  
 PUBMED [10074091](#)  
 REFERENCE 2 (residues 1 to 740)  
 AUTHORS Nehls, U.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-AUG-1998) Nehls U., Universitaet Tuebingen,  
 Botanisches Institut, Physiologische Oekologie der Pflanzen, Auf  
 der Morgenstelle 1, Tuebingen 72076, GERMANY  
 FEATURES Location/Qualifiers  
 source 1..740  
 /organism="Amanita muscaria"  
 /db\_xref="taxon:[41956](#)"  
 Protein 1..740  
 /product="phenylalanine ammonium lyase"  
 CDS 1..740  
 /gene="PAL"  
 /coded\_by="AJ010143.1:18..2240"  
 /db\_xref="GOA:O93967"  
 /db\_xref="InterPro:[IPR001106](#)"  
 /db\_xref="InterPro:[IPR005922](#)"  
 /db\_xref="InterPro:[IPR008948](#)"  
 /db\_xref="UniProt/Swiss-Prot:[O93967](#)"

## ORIGIN

```

  1 mgldnsknta kffdlpkavh gmngttpvng fkatalskas rtmtktsals qfleayrele
  61 gykngraikv dgqtlsiaav aaaaryaav eldesplvke rvrksqlaia nkvstgasvy
  121 glstgfggsa dtrtdkpml1 gfallqhghv gilptstepl dvlplqdan tsmpeawirg
  181 ailirmnsli rghsgirwel iekmrrellaa nvipvvplrg sisssgd lsp lsyiaigtig
  241 npsikvhgpg sksgirqigs skdvlalhni epfpleskep lgilngtafs asvaalalne
  301 aihlvllaqv ctamgteali gtrashapfi hatarphpgq vecaeniwnl ldgsklaqe
  361 ehevrleddk ytlrqdrypl rtspqflgpq iediisafqt vtqecnylpa tdnplidjet
  421 geshhggnfq amavtnamek trlalhhvgk llfsqstelv npamnrglpp svaatdpsln

```

481 yhakgldiat aayvaeatpg pthiqsaemh nqavnslali saratitsle vltsliasyl  
541 yilcqaldlr alqreflpgl diireelrs sfgsflsseq meklqgnlts afedhldktt  
601 tmdndrmtt maatsssvll qfftdsgasv ppssccllss vssfqssvat rssvlmddlr  
661 keyifgdrgp tpasqyigkt rpvyqfirtt igvrkhgsen ynkfynglgv edvtiggnis  
721 riyesirdgk mqsiivsffd

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

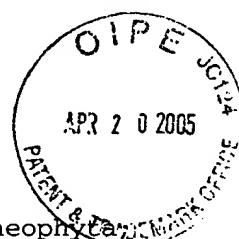
Limits Preview/Index History Clipboard Details

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

1: AAC18871. Reports phenylalanine amm...[gi:497421]

BLink, Domains,  
Links

LOCUS AAC18871 717 aa linear PLN 04-JUN-1998  
 DEFINITION phenylalanine ammonia lyase [Arabidopsis thaliana].  
 ACCESSION AAC18871  
 VERSION AAC18871.1 GI:497421  
 DBSOURCE locus ATHPAL2 accession L33678.1  
 KEYWORDS .  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (residues 1 to 717)  
 REFERENCE Wanner, L.A., Li, G., Ware, D., Somssich, I.E. and Davis, K.R.  
 AUTHORS  
 TITLE The phenylalanine ammonia-lyase gene family in Arabidopsis thaliana  
 JOURNAL Plant Mol. Biol. 27 (2), 327-338 (1995)  
 PUBMED 7888622  
 COMMENT Method: conceptual translation.  
 FEATURES Location/Qualifiers  
 source 1..717  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia"  
 /db\_xref="taxon:3702"  
 /tissue\_lib="MboI partial digestion in lambda EMBL4"  
Protein 1..717  
 /product="phenylalanine ammonia lyase"  
 /EC\_number="4.3.1.5"  
CDS 1..717  
 /gene="PAL2"  
 /coded\_by="join(L33678.1:1466..1869,L33678.1:2080..3829)"  
 ORIGIN  
 1 mdqieamlcg ggektkvav tktladplnw glaadqmkg s h l d e v k k m v e e y r r p v v n l g  
 61 getltigqva aistvggsvk velaetsrag v k a s s d w v m e s m n k g t d s y g v t t g f g a t s h  
 121 r r t k n g t a l q t e l i r f l n a g i f g n t k e t c h t l p q s a t r a a m l v r v n t l l q g y s g i r f e i l  
 181 e a i t s l l n h n i s p s l p l r g t i t a s g h l v p l s y i a g l l t g r p n s k a t g p d g e s l t e k e a f e  
 241 k a g i s t g f f d l q p k e g l a l v n g t a v g s g m a s m v l f e a n v q a v l a e v l s a i f a e v m s g k p e  
 301 f t d h l t h r l k h h p g q i e a a a i m e h i l d g s s y m k l a q k v h e m d p l q k p k q d r y a l r t s p q w  
 361 l g p q i e v i r q a t k s i e r e i n s v n d n p l i d v s r n k a i h g g n f q g t p i g v s m d n t r l a i a a i  
 421 g k l m f a q f s e l v n d f y n n g l p s n l t a s s n p s l d y g f k g a e i a m a s y c s e l q y l a n p v t s h  
 481 v q s a e q h n q d v n s l g l i s s r k t s e a v d i l k l m s t t f l v g i c q a v d l r h l e e n l r q t v k n t  
 541 v s q v a k k v l t t g i n g e l h p s r f c e k d l l k v v d r e q v f t y v d d p c s a t y p l m q r l r q v i v d  
 601 h a l s n g e t e k n a v t s i f q k i g a f e e e l k a v l p k e v e a a r a a y g n g t a p i p n r i k e c r s y p  
 661 l y r f v r e e l g t k l l t g e k v v s p g e e f d k v f t a m c e g k l i d p l m d c l k e w n g a p i p i c  
 //



[Disclaimer](#) | [Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein**  for  **Go** **Clear**

Limits Preview/Index History Clipboard Details

**Display** GenPept  all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**P45730: Reports Phenylalanine amm...[gi:1172001]**

BLink, Domains, Links

LOCUS P45730 715 aa linear PLN 01-MAY-2005

DEFINITION Phenylalanine ammonia-lyase.

ACCESSION P45730

VERSION P45730 GI:1172001

DBSOURCE swissprot: locus PALY\_POPTR, accession P45730;

class: standard.

created: Nov 1, 1995.

sequence updated: Nov 1, 1995.

annotation updated: May 1, 2005.

xrefs: L11747.1, AAA33805.1

xrefs (non-sequence databases): HSSPP21310, InterProIPR008948, InterProIPR001106, InterProIPR005922, PfamPF00221, TIGRFAMsTIGR01226, PROSITEPS00488

KEYWORDS Lyase; Multigene family; Phenylpropanoid metabolism.

SOURCE Populus trichocarpa (Populus balsamifera subsp. trichocarpa)

ORGANISM Populus trichocarpa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.

REFERENCE 1 (residues 1 to 715)

AUTHORS Subramaniam,R., Reinold,S., Molitor,E.K. and Douglas,C.J.

TITLE Structure, inheritance, and expression of hybrid poplar (*Populus trichocarpa* x *Populus deltoides*) phenylalanine ammonia-lyase genes

JOURNAL Plant Physiol. 102 (1), 71-83 (1993)

PUBMED 8108506

REMARK NUCLEOTIDE SEQUENCE.

COMMENT STRAIN=P.trichocarpa X P.deltoides; TISSUE=Leaf

[FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton.

[CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH<sub>3</sub>.

[PATHWAY] Phenylpropanoid biosynthesis; first step.

[SUBCELLULAR LOCATION] Cytoplasmic (Probable).

[PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity).

[SIMILARITY] Belongs to the PAL/histidase family.

FEATURES Location/Qualifiers

source 1..715  
           /organism="Populus trichocarpa"  
           /db\_xref="taxon:3694"

gene 1..715  
       /gene="PAL"

Protein 1..715  
       /gene="PAL"



Bond  
/product="Phenylalanine ammonia-lyase"  
/EC\_number="4.3.1.5"  
bond(201,203)  
/gene="PAL"  
/bond\_type="xlink"  
/note="5-imidazolinone (Ala-Gly) (By similarity)."  
/evidence=not\_experimental  
Site  
202  
/gene="PAL"  
/site\_type="modified"  
/note="2,3-didehydroalanine (Ser) (By similarity)."  
/evidence=not\_experimental  
ORIGIN  
1 metvtkngyq ngsleslcvn qrdplswgva aeamkgshld evkrmvadyr kpvvklgget  
61 ltiaqvasia ghdtdgvkve lsesarpgvk assdwwmdsm dkgttsygvt tgfgatshrr  
121 tkqggalqke lirflnagif gngtetcctl phsattraaml vrintllqgy sgirfeilea  
181 itrlnnnnit pclplrgtit asgdlvpls iaglltgrpn skatgptgev ldaaeafkaa  
241 giesgffelq pkeglalvng tavgsglasm vlfetnvlav lsellsaifa evmngkpeft  
301 dhlthklkh pgqieaaaaim ehildgsaym kaakkhetd plqkpkqdry alrtspqwlg  
361 pqievirfst ksiereinsv ndnplidvsr nkaihggnfq gtpigvsmdn vrlaiasigm  
421 llfaqfselv ndfyngnlps nltasrnpsl dygfkgaeia masycselqy lanpvtthvq  
481 saeqhnqdvn slglissrkt aeavdilkml sttfivalcq aidlrhleen lksavkntvs  
541 qvskrvlttg angelhpsrf cekellkvvd reyvfayvdd pcsatyplmq klrqvfvdha  
601 lengeneknf stsvfqkiae feeelkallp kevesaraay dsgnsaidnk ikecrsyply  
661 kfvreelgtv lltgekvqsp geefdkvfta mcqgkiidpm leclgewngs plpic  
//

[Disclaimer](#) | [Write to the Help Desk](#)  
NCBI | NLM | NIH

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein**  for

Limits Preview/Index History Clipboard Details

**Display** GenPept  all to file

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

1: [O64963. Reports Phenylalanine amm...\[gi:6647711\]](#) [BLink](#), [Domains](#), [Links](#)

**LOCUS** O64963 717 aa linear PLN 01-MAY-2005  
**DEFINITION** Phenylalanine ammonia-lyase 1.  
**ACCESSION** O64963  
**VERSION** O64963 GI:6647711  
**DBSOURCE** swissprot: locus PAL1\_PRUAV, accession [O64963](#);  
 class: standard.  
 created: May 30, 2000.  
 sequence updated: May 30, 2000.  
 annotation updated: May 1, 2005.  
 xrefs: [AF036948.1](#), [AAC78457.1](#)  
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,  
 InterProIPR001106, InterProIPR005922, PfamPF00221,  
 TIGRFAMsTIGR01226, PROSITEPS00488

**KEYWORDS** Lyase; Multigene family; Phenylpropanoid metabolism.  
**SOURCE** Prunus avium (sweet cherry)  
**ORGANISM** [Prunus avium](#) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

**REFERENCE** 1 (residues 1 to 717)  
**AUTHORS** Wiersma, P.A. and Wu, Z.  
**TITLE** A full-length cDNA for phenylalanine ammonia-lyase cloned from ripe Sweet Cherry fruit (Prunus avium)  
**JOURNAL** Unpublished  
**REMARK** NUCLEOTIDE SEQUENCE.  
**COMMENT** STRAIN=cv. Summit  
 [FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton.  
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH<sub>3</sub>.  
 [PATHWAY] Phenylpropanoid biosynthesis; first step.  
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).  
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity).  
 [SIMILARITY] Belongs to the PAL/histidase family.

**FEATURES** Location/Qualifiers  
**source** 1..717  
 /organism="Prunus avium"  
 /db\_xref="taxon:42229"  
**gene** 1..717  
 /gene="PAL1"  
**Protein** 1..717  
 /gene="PAL1"  
 /product="Phenylalanine ammonia-lyase 1"



Bond

```
/EC_number="4.3.1.5"
bond(203,205)
/gene="PAL1"
/bond_type="xlink"
/note="5-imidazolinone (Ala-Gly) (By similarity)."
/evidence=not_experimental
```

Site

```
204
/gene="PAL1"
/site_type="modified"
/note="2,3-didehydroalanine (Ser) (By similarity)."
/evidence=not_experimental
```

## ORIGIN

```
1 matnsikqng hkngsvelpe lcikkdpnlw gvaaetlkgs hldevkrmvva eyrkpvvkglg
61 gesltisqva aiathdsgvk velsesarag vkassdwvmd smskgtdsyg vttgfgatsh
121 rrtkqgaalq kelirflnag vfgstkesgh tlphqatrraa mlvrintllq gysgirfeil
181 evitkflnnn vtpclplrgt itasgdlvpl syiagmltgr pnskavgpdg qtlsaaeafe
241 fvginsgffe lqpkeglalv ngtavgsbla stvlfdtnil allseilsai faevmqgkpe
301 ftdhlthklk hhpqgieaaa imehildgss yvkaakkhe qdplqkpkqd ryalrtspqw
361 lgpqieviry stksiereid svndnplidv srnkahggn fqqtpigvsm dntrlaiasi
421 gklmfaqfse lvndfynngl psnlsggrnp sldygfkgae iamasycsel qflanpvtvh
481 vqsaeqhnhqd vnslgliissr ktaeavdilk lmsstflval cqaidlrhle enlrvtknt
541 vsqvakrtlt tgvngelhps rfcekdllkv vdreyvfayi ddpcsatypl mqklrqvlive
601 haltngebek nastsifqki vafeeekvl lpkevdsara aldsagsagvp nrtecrsyp
661 lykfvreelg aeyltgekvr spgeecdkvf taicegkiid pildclegwn gaplic
```

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

**Display** GenPept  Send  all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**P 1: P45732. Reports Phenylalanine amm...[gi:1172002]**

[BLink, Domains, Links](#)

**LOCUS** P45732 715 aa linear PLN 01-MAY-2005  
**DEFINITION** Phenylalanine ammonia-lyase.  
**ACCESSION** P45732  
**VERSION** P45732 GI:1172002  
**DBSOURCE** swissprot: locus PALY\_STYHU, accession [P45732](#);  
 class: standard.  
 created: Nov 1, 1995.  
 sequence updated: Nov 1, 1995.  
 annotation updated: May 1, 2005.  
 xrefs: [L36822.1](#), [AAA99500.1](#)  
 xrefs (non-sequence databases): HSSPP21310, InterProIPR008948,  
 InterProIPR001106, InterProIPR005922, PfamPF00221,  
 TIGRFAMsTIGR01226, PROSITEPS00488  
**KEYWORDS** Lyase; Phenylpropanoid metabolism.  
**SOURCE** Stylosanthes humilis (Townsville stylo)  
**ORGANISM** [Stylosanthes humilis](#)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
 Aeschynomeneae; Stylosanthes.  
**REFERENCE** 1 (residues 1 to 715)  
**AUTHORS** Manners,J.M., McIntyre,C.L. and Nourse,J.P.  
**TITLE** Cloning and sequence of a cDNA encoding phenylalanine ammonia-lyase  
 from the tropical forage legume *Stylosanthes humilis*  
**JOURNAL** Plant Physiol. 108 (3), 1301-1302 (1995)  
**PUBMED** [7630950](#)  
**REMARK** NUCLEOTIDE SEQUENCE.  
 STRAIN=cv. Paterson; TISSUE=Stem  
**COMMENT** [FUNCTION] This is a key enzyme of plant metabolism catalyzing the  
 first reaction in the biosynthesis from L-phenylalanine of a wide  
 variety of natural products based on the phenylpropane skeleton.  
 [CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH<sub>3</sub>.  
 [PATHWAY] Phenylpropanoid biosynthesis; first step.  
 [SUBCELLULAR LOCATION] Cytoplasmic (Probable).  
 [PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO),  
 which is formed autocatalytically by cyclization and dehydration of  
 residues Ala-Ser-Gly (By similarity).  
 [SIMILARITY] Belongs to the PAL/histidase family.  
**FEATURES** Location/Qualifiers  
**source** 1..715  
 /organism="Stylosanthes humilis"  
 /db\_xref="taxon:[35628](#)"  
**gene** 1..715  
 /gene="PAL17.1"  
**Protein** 1..715

Bond  
/gene="PAL17.1"  
/product="Phenylalanine ammonia-lyase"  
/EC\_number="4.3.1.5"  
bond(201,203)  
/gene="PAL17.1"  
/bond\_type="xlink"  
/note="5-imidazolinone (Ala-Gly) (By similarity)."  
/evidence=not\_experimental  
Site  
202  
/gene="PAL17.1"  
/site\_type="modified"  
/note="2,3-didehydroalanine (Ser) (By similarity)."  
/evidence=not\_experimental

## ORIGIN

1 mdthanadat fcltanngqq prhdplnwaa aaealkgsh1 devkrmvsey rkplvnlggq  
61 tltisqvaai aandqgvsvq lseasragvk assdwvmdsm nnngtdsygvt tgfgatshrr  
121 tkqggalqke lirflnagif gngtetcnctl phtatraaml vrintllqgy sgirfeilea  
181 itkllnnnit pclplrgtit asgdlvplsya iaglltgrpn skavgpnget lnakafeafqaa  
241 gigsdffelq pkeglalvng tpvgsglasv vlfeanilav lsevlsaiifa evmqgkpeft  
301 dhlthklkh pgqieaaaaim ehildgssyv kaakkheid plqpkpqdry alrtspqwlg  
361 plvevirfst ksiereinsv ndnplidvsr nkalhgnfq gtpigvsmdn trlavasigk  
421 lmfaqfselv ndfyngnlps nlsasrnplsl dygfkgteia masycselqy lanpvtshvq  
481 saeqhnqdvn slglisarkt neaveilkml sptylialcq aidlrhleen lkntvkntvs  
541 qvakrtlttg vngelhpsrf cekd11kivd reycfayidd pcsatyplmq klrqvlveha  
601 lanaeneknv ntsifqkitt feeelktllp kevegariay engqsaipnk ikecrsyply  
661 kfvrreelgte mltgekvrsp geecdklfta mcqgkiidpl lecigewnga plplc

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

**Display** GenPept  all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**P 1: P45734. Reports Phenylalanine amm...[gi:1172003]**

BLink, Domains, Links

**LOCUS** P45734 725 aa linear PLN 01-MAY-2005

**DEFINITION** Phenylalanine ammonia-lyase.

**ACCESSION** P45734

**VERSION** P45734 GI:1172003

**DBSOURCE** swissprot: locus PALY\_TRISU, accession [P45734](#); class: standard. created: Nov 1, 1995. sequence updated: Nov 1, 1995. annotation updated: May 1, 2005. xrefs: [M91192.1](#), [AAA17993.1](#) xrefs (non-sequence databases): HSSPP21310, InterProIPR008948, InterProIPR001106, InterProIPR005922, PfamPF00221, TIGRFAMsTIGR01226, PROSITEPS00488

**KEYWORDS** Lyase; Multigene family; Phenylpropanoid metabolism.

**SOURCE** Trifolium subterraneum

**ORGANISM** [Trifolium subterraneum](#) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trifolium.

**REFERENCE** 1 (residues 1 to 725)

**AUTHORS** Howles, P.A., Arioli, T. and Weinman, J.J.

**TITLE** Characterization of a phenylalanine ammonia-lyase multigene family in [Trifolium subterraneum](#)

**JOURNAL** Gene 138 (1-2), 87-92 (1994)

**PUBMED** 8125321

**REMARK** NUCLEOTIDE SEQUENCE.  
STRAIN=cv. Karridale; TISSUE=Leaf  
[FUNCTION] This is a key enzyme of plant metabolism catalyzing the first reaction in the biosynthesis from L-phenylalanine of a wide variety of natural products based on the phenylpropane skeleton.  
[CATALYTIC ACTIVITY] L-phenylalanine = trans-cinnamate + NH<sub>3</sub>.  
[PATHWAY] Phenylpropanoid biosynthesis; first step.  
[SUBCELLULAR LOCATION] Cytoplasmic (Probable).  
[PTM] Contains an active site 4-methylidene-imidazole-5-one (MIO), which is formed autocatalytically by cyclization and dehydration of residues Ala-Ser-Gly (By similarity).  
[SIMILARITY] Belongs to the PAL/histidase family.

**FEATURES** Location/Qualifiers

**source** 1..725 /organism="Trifolium subterraneum"  
/db\_xref="taxon:3900"

**gene** 1..725 /gene="PAL1"

**Protein** 1..725



Bond  
`/gene="PAL1"  
/product="Phenylalanine ammonia-lyase"  
/EC_number="4.3.1.5"  
bond(211,213)  
/gene="PAL1"  
/bond_type="xlink"  
/note="5-imidazolinone (Ala-Gly) (By similarity)."  
/evidence=not_experimental`

Site  
`212  
/gene="PAL1"  
/site_type="modified"  
/note="2,3-dihydroalanine (Ser) (By similarity)."  
/evidence=not_experimental`

ORIGIN  
`1 mevvaailk nnindydsfc lthanannmk vnaadplnwg vaaeamkgsh ldevkrmvee  
61 yrkpvvrlgg etltisgvaa iaahdgatve lsesaragvk assdwvmesm nkgtdsygvt  
121 tgfagtshrr tkqggalqke lirflnagif gngtesnhtl phtatraaml vrintllqgy  
181 sgirfeilea itkllnnnit polplrgtit asgdlvpalsy iaglltgrsn skahgpsgem  
241 lnakeafqla ginaeffelq pkeglalvng tavgsglassi vlfeanilav lsevlsaifa  
301 evmqgkpeft dhlthklkh pgqieaaaim ehilhgsayv kdakkhemd plqkpkqdry  
361 alrtspqwlg plievirst ksiereinsv ndnplidvsr nkalhggnfq gtpigvsmdn  
421 trlalasigk llfaqfselv ndfyngnlps nlsasrnpsl dygfkgseia masycselqy  
481 lanpvtthvq saeqhnqdv slglissrkt keaieilqlm sstfialcq aidlrhleen  
541 lknsvkntvs qvakktltig vsgelhpsrf cekd1lkvvd rehvfsyidd pcsatyplaq  
601 klrqvldha lvngesekns ntsifqkiat feeelktllp kevesartay engnstiank  
661 ingcrsyply kfvrreelgts lltgervisp geecdklfta mcqgkiidpl lkclgewnga  
721 plpic`

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI**   **Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for

Limits Preview/Index History Clipboard Details

Range: from  to  Features:  SNP  CDD  MGC  HPRD  STS

1: [CAA05251](#). Reports phenylalanine amm...[gi:2631995]

BLink, Domains,  
Links

LOCUS CAA05251 713 aa linear PLN 15-APR-2005  
**DEFINITION** phenylalanine ammonia lyase [Digitalis lanata].  
**ACCESSION** CAA05251  
**VERSION** CAA05251.1 GI:2631995  
**DBSOURCE** embl locus DLJ002221, accession [AJ002221.1](#)  
**KEYWORDS** .  
**SOURCE** Digitalis lanata  
**ORGANISM** Digitalis lanata  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 asterids; lamiids; Lamiales; Plantaginaceae; Digitalideae;  
 Digitalis.  
**REFERENCE** 1 (residues 1 to 713)  
**AUTHORS** Thoeringer,C.  
**JOURNAL** Unpublished  
**REFERENCE** 2 (residues 1 to 713)  
**AUTHORS** Thoeringer,C.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (14-NOV-1997) Thoeringer C., Institute of Pharmaceutical  
 Biology, Martin-Luther-University Halle, Hoher Weg 7, D-06120,  
 GERMANY  
**FEATURES** Location/Qualifiers  
**source**  
 1..713  
 /organism="Digitalis lanata"  
 /db\_xref="taxon:[49450](#)"  
 /clone\_lib="Lambda ZAP"  
 /dev\_stage="leaves"  
**Protein**  
 1..713  
 /product="phenylalanine ammonia lyase"  
**CDS**  
 1..713  
 /coded\_by="AJ002221.1:124..2265"  
 /db\_xref="GOA:O23924"  
 /db\_xref="InterPro:[IPR001106](#)"  
 /db\_xref="InterPro:[IPR005922](#)"  
 /db\_xref="InterPro:[IPR008948](#)"  
 /db\_xref="UniProt/Swiss-Prot:[O23924](#)"

**ORIGIN**

```

1 maavvenghh gnngfcvkqn dplnwvaaae elkgshldev krmveefrkt vvklggetlt
61 isqvaaiar dnevavqlae ssragvkass dwvmesmnkg tdsygvttgf gatshrrtkq
121 ggalqkelir flnagifgng testhtlphs atraamlvri ntllqgysgi rfeiletitk
181 flnhnitpcl plrgtitasg dlvplesyiag lltgrpnska vgpngeslna eqafklagan
241 sglffelqpk eglalvngta vgsglasial yeanilslla evmsavfaev mngkpeftdh
301 lthklkhpg qieaaaimeh ildgssyvka aqkmhemdpl qkpkqdryal rtspqwlgpq
361 ievirtatkm iereinsvnd nplidvsrnk alhggnfqgt pigvsmdnsr laiasigklm
421 faqfselvnd fynnglpsnl sggrnpsldy gfkgsiama sycselqfla npvtvhvqsa

```

481 eqhnqdvns1 glissrktve aldilklmss tylvalcqai dlrhleenlr lsvkntisqv  
541 akrtlttgvn gelhpsrfce ldllrvvdre yvfayvddpc satyplmgkl rqvlvehalk  
601 ngeneknast sifqkieafe aelkavlpke vesarvaled gkpaianrit ecrsyplykf  
661 ireelgtnfl tgekvmspge ecdrvftams kglivdp1lk clegwngapl pic

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

**NCBI Protein**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Protein** for **Go** **Clear**

Limits Preview/Index History Clipboard Details

**Display** GenPept **Send** all to file

Range: from **begin** to **end** Features:  SNP  CDD  MGC  HPRD  STS

**1: CAA37129. Reports phenylalanine amm...[gi:18377]**

BLINK, Domains, Links

LOCUS CAA37129 713 aa linear PLN 18-AUG-1993

DEFINITION phenylalanine ammonia-lyase [Glycine max].

ACCESSION CAA37129

VERSION CAA37129.1 GI:18377

DBSOURCE embl locus DMPAL1, accession x52953.1

KEYWORDS .

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (residues 1 to 713)

AUTHORS Frank, R.L. and Vodkin, L.O.

TITLE Sequence and structure of a phenylalanine ammonia-lyase gene from Glycine max

JOURNAL DNA Seq. 1 (5), 335-346 (1991)

PUBMED 1799682

REFERENCE 2 (residues 1 to 713)

AUTHORS Frank, R.L.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-1990) Frank R.L., University of Missouri-Rolla, Life Sciences Department, 105 Schrenk Hall, Rolla, Missouri 65401, U.S.A

FEATURES Location/Qualifiers

source 1..713  
           /organism="Glycine max"  
           /strain="T225"  
           /db\_xref="taxon:3847"  
           /clone="lambda P10"  
           /tissue\_type="leaf"  
           /clone\_lib="lambda charon 35"

Protein 1..713  
           /product="phenylalanine ammonia-lyase"  
           /EC\_number="4.3.1.5"

CDS 1..713  
       /gene="PAL1"  
       /coded\_by="join(X52953.1:189..580,X52953.1:2100..3849)"  
       /db\_xref="GOA:P27991"  
       /db\_xref="UniProt/Swiss-Prot:P27991"

ORIGIN

```

 1 meatnghqng sfclstakgn ndplnwgaaa eamkgshlde vkrmvaaeyrk pvvrlggetl
 61 tiaqvaavag hdhgavvels esaregvkas sewvmnsmnn gtdsygvttg fgatshrrtk
121 qgalqkeli rflnagifgn gtesshtlph tatraamlvr intllggysg irfeileait
181 k1lnnnvtpc ldlrgtitas gdlvplsyia glltgrpnsk avgpsgevln akeafelasi

```

241 nseffelqpk eglalvngta vgsglasmvl feanilavls evlsaifaev mqgkpeftdh  
301 lthklkhpg qieaaaimeh ildgssymka akklheidpl qkpkqdryal rtspqwlqp1  
361 ievirfstks iereinsvnd nplidvsrnk alhggnfqgt pigvsmdntr lalasigklm  
421 faqfselvnd fynnglpsnl tasrnpsldy gfkgaeiama sycselqyla npvtthvqsa  
481 eqhnqdvns1 glissrktne aieilkmlss tflialcqai dlrhleenlk nsvkntvsqv  
541 skrilttgvm gelhpsrfce kdllkvvdre yifsyiddpc satyplmqkl rqvlvdhalv  
601 naecekdvns sifqkiaife eelknllpke vegaraayes gkaaipnkiq ecrsyplykf  
661 vreelgtgll tgekvrspge efdklftamc qgkiidplme clgewngapl pis

//

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10